

**WEST Search History**

10/7/4,389

Hide Items

Restore

Clear

Cancel

DATE: Thursday, October 12, 2006

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L9	20030027988	1
<input type="checkbox"/>	L8	20030022334	1
		<i>DB=USPT; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L7	5654172.pn.	1
<input type="checkbox"/>	L6	6531297.pn.	1
<input type="checkbox"/>	L5	6943241.pn.	1
<input type="checkbox"/>	L4	6783969.pn.	1
		<i>DB=PGPB; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L3	20040259086	1
<input type="checkbox"/>	L2	20040132087	1
<input type="checkbox"/>	L1	2004132087	0

END OF SEARCH HISTORY

**SCORE Search Results Details for Application 10714389 and Search Result us-10-714-389-52.rge.**

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OM nucleic - nucleic search, using sw model

```
Run on:      October  3, 2006, 18:50:57 ; Search time 3928 Seconds
              (without alignments)
              6170.080 Million cell updates/sec
```

Title: US-10-714-389-52  
Perfect score: 379  
Sequence: 1 actttgccaagcagtaaagg.....ttcaggtatgagtcagggt 379

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	379	100.0	379	2	CS110385	CS110385 Sequence
2	379	100.0	379	2	AX156195	AX156195 Sequence
c 3	379	100.0	397	2	CQ421094	CQ421094 Sequence
4	379	100.0	403	2	CQ426106	CQ426106 Sequence
c 5	379	100.0	598	2	CQ492564	CQ492564 Sequence
c 6	379	100.0	598	2	CQ496194	CQ496194 Sequence
c 7	379	100.0	963	2	CS110636	CS110636 Sequence
c 8	379	100.0	1518	2	CS110638	CS110638 Sequence
c 9	379	100.0	1548	2	CS110645	CS110645 Sequence
c 10	379	100.0	1586	2	AX195182	AX195182 Sequence
c 11	379	100.0	1598	2	CS110635	CS110635 Sequence
c 12	379	100.0	1894	2	AX829108	AX829108 Sequence
c 13	379	100.0	1907	5	AY262056	AY262056 Homo sapi
c 14	379	100.0	2015	2	CS110637	CS110637 Sequence
c 15	379	100.0	2015	2	AX317983	AX317983 Sequence
c 16	379	100.0	2020	2	CQ970464	CQ970464 Sequence
c 17	379	100.0	2020	2	AX358776	AX358776 Sequence
c 18	379	100.0	2020	2	AX362269	AX362269 Sequence
c 19	379	100.0	2020	5	AY358631	AY358631 Homo sapi
c 20	377.4	99.6	386	2	CQ430462	CQ430462 Sequence
c 21	377.4	99.6	393	2	CQ418480	CQ418480 Sequence
c 22	377.4	99.6	393	2	CQ421061	CQ421061 Sequence
c 23	377.4	99.6	393	2	CQ426250	CQ426250 Sequence
c 24	372	98.2	651	2	CQ421181	CQ421181 Sequence
c 25	369.4	97.5	792	2	CQ430054	CQ430054 Sequence
c 26	367	96.8	392	2	CQ429968	CQ429968 Sequence
c 27	365.4	96.4	392	2	CQ429935	CQ429935 Sequence
28	365.4	96.4	397	2	CQ421574	CQ421574 Sequence
29	363	95.8	393	2	CQ430100	CQ430100 Sequence
30	363	95.8	415	2	CQ421229	CQ421229 Sequence
c 31	363	95.8	1436	5	AY262057	AY262057 Homo sapi
c 32	363	95.8	2608	2	CS168612	CS168612 Sequence
c 33	363	95.8	2608	2	AX834733	AX834733 Sequence
c 34	363	95.8	2608	5	AK097373	AK097373 Homo sapi
c 35	361.4	95.4	392	2	CQ426196	CQ426196 Sequence
c 36	357.2	94.2	1503	2	AX768910	AX768910 Sequence
37	356	93.9	422	2	CQ418336	CQ418336 Sequence
c 38	342.4	90.3	357	2	CQ421595	CQ421595 Sequence
c 39	329.4	86.9	364	2	CQ426051	CQ426051 Sequence
c 40	317.6	83.8	391	2	CQ417373	CQ417373 Sequence
c 41	313.8	82.8	396	2	CQ418426	CQ418426 Sequence
42	312.4	82.4	318	2	CQ430441	CQ430441 Sequence
c 43	253.6	66.9	1197	5	AY696295	AY696295 Homo sapi
44	235.2	62.1	444	2	CQ505007	CQ505007 Sequence
45	235.2	62.1	444	2	CQ510749	CQ510749 Sequence

## ALIGNMENTS

RESULT 1  
CS110385

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OM nucleic - nucleic search, using sw model

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Run on:      October 3, 2006, 18:33:05 ; Search time 521 Seconds
              (without alignments)
              5071.943 Million cell updates/sec
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Title: US-10-714-389-52  
Perfect score: 379  
Sequence: 1 actttgccaaagcagtaaaag.....ttcaggtatgagtcagggt 379

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

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Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	379	100.0	379	4	AAH55527	Aah55527 Human bre
2	379	100.0	379	7	ADU01271	Adu01271 Breast ca
3	379	100.0	379	7	ADZ41535	Adz41535 Human bre
4	379	100.0	379	12	ADN40297	Adn40297 Human bre
c 5	379	100.0	397	4	AAL13663	Aal13663 Human bre
6	379	100.0	403	4	AAL18673	Aal18673 Human bre
c 7	379	100.0	598	5	ABV24442	Abv24442 Human pro
c 8	379	100.0	598	5	ABV28048	Abv28048 Human pro
c 9	379	100.0	870	11	ACN83733	Acn83733 Breast ca
c 10	379	100.0	963	7	ADU01522	Adu01522 Breast ca
c 11	379	100.0	963	7	ADZ41786	Adz41786 Human bre
c 12	379	100.0	1299	11	ACN89634	Acn89634 Breast ca
c 13	379	100.0	1518	7	ADU01524	Adu01524 Breast ca
c 14	379	100.0	1518	7	ADZ41788	Adz41788 Human bre
c 15	379	100.0	1518	12	ADQ48399	Adq48399 Human cyt
c 16	379	100.0	1586	4	AAD09946	Aad09946 Human dru
c 17	379	100.0	1598	7	ADU01521	Adu01521 Breast ca
c 18	379	100.0	1598	7	ADZ41785	Adz41785 Human bre
c 19	379	100.0	1743	12	ADJ67057	Adj67057 Human sec
c 20	379	100.0	1894	6	ABT07693	Abt07693 Breast ca
c 21	379	100.0	1906	12	ADQ36612	Adq36612 Human CYP
c 22	379	100.0	1975	10	AAD60551	Aad60551 Human cyt
c 23	379	100.0	1975	10	ACA61906	Aca61906 cDNA enco
c 24	379	100.0	1975	12	ADQ48397	Adq48397 Human cyt
c 25	379	100.0	2015	6	AAD24015	Aad24015 Human dru
c 26	379	100.0	2015	7	ADU01523	Adu01523 Breast ca
c 27	379	100.0	2015	7	ADZ41787	Adz41787 Human bre
c 28	379	100.0	2020	6	ABK33550	Abk33550 cDNA enco
c 29	379	100.0	2020	7	ADY31769	Ady31769 Novel hum
c 30	379	100.0	2020	8	ACA68511	Aca68511 Novel hum
c 31	379	100.0	2020	9	ABT44240	Abt44240 Human PRO
c 32	379	100.0	2020	9	ABT44523	Abt44523 Human PRO
c 33	379	100.0	2020	9	ACD82190	Acd82190 Human sec
c 34	379	100.0	2020	9	ABT43896	Abt43896 Human mem
c 35	379	100.0	2020	9	ADB83519	Adb83519 Novel hum
c 36	379	100.0	2020	9	ADB80625	Adb80625 Novel hum
c 37	379	100.0	2020	9	ADB73166	Adb73166 Novel hum
c 38	379	100.0	2020	9	ADB78248	Adb78248 Novel hum
c 39	379	100.0	2020	10	ADB84896	Adb84896 Human PRO
c 40	379	100.0	2020	10	ADB78002	Adb78002 Novel hum
c 41	379	100.0	2020	10	ADB87068	Adb87068 Human PRO
c 42	379	100.0	2020	10	ADB84650	Adb84650 Human PRO
c 43	379	100.0	2020	10	ADB83765	Adb83765 Novel hum
c 44	379	100.0	2020	10	ADB72920	Adb72920 Novel hum
c 45	379	100.0	2020	10	ADC36758	Adc36758 Human PRO

## ALIGNMENTS

RESULT 1  
AAH55527

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OM nucleic - nucleic search, using sw model

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Run on:      October 3, 2006, 19:17:32 ; Search time 154 Seconds
              (without alignments)
              4604.872 Million cell updates/sec
```

Title: US-10-714-389-52  
Perfect score: 379  
Sequence: 1 actttgccaaqcgagtaaagg.....ttcaggtatgagtcagggt 379

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

```
Minimum DB seq. length: 0
Maximum DB seq. length: 2000000000
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```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Issued_Patents_NA:*
1:  /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2:  /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3:  /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5:  /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7:  /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result			%		Query		DB	ID	Description
			Score	Match	Length				
c	1	154.6	40.8	1508	3	US-09-799-451-109			Sequence 109, App
c	2	154.6	40.8	2071	3	US-10-104-047-720			Sequence 720, App
c	3	154.6	40.8	2327	3	US-09-852-067-1			Sequence 1, Appli
c	4	154.6	40.8	2327	3	US-10-338-691-1			Sequence 1, Appli
c	5	153	40.4	1718	3	US-09-799-451-420			Sequence 420, App
c	6	111.4	29.4	2084	3	US-09-023-655-1045			Sequence 1045, Ap
c	7	98.4	26.0	2382	3	US-09-023-655-1436			Sequence 1436, Ap
c	8	96.8	25.5	2576	4	US-09-880-107-2138			Sequence 2138, Ap
c	9	82.6	21.8	1763	4	US-09-880-107-1610			Sequence 1610, Ap
c	10	73.4	19.4	300	3	US-09-172-108-2			Sequence 2, Appli
c	11	73.4	19.4	300	3	US-09-172-711-3			Sequence 3, Appli
c	12	69.8	18.4	1634	5	US-10-114-270-59			Sequence 59, Appl
c	13	69.8	18.4	1669	3	US-09-976-594-532			Sequence 532, App
c	14	66.6	17.6	2227	3	US-09-023-655-1433			Sequence 1433, Ap
c	15	66.4	17.5	888	3	US-09-023-655-198			Sequence 198, App
c	16	66.4	17.5	1676	3	US-09-991-181-263			Sequence 263, App
c	17	66.4	17.5	1676	3	US-09-990-444-263			Sequence 263, App
c	18	66.4	17.5	1676	3	US-09-997-333-263			Sequence 263, App
c	19	66.4	17.5	1676	3	US-09-992-598-263			Sequence 263, App
c	20	66.4	17.5	1676	4	US-09-989-735-263			Sequence 263, App
c	21	66.4	17.5	1676	5	US-09-989-726-263			Sequence 263, App
c	22	66.4	17.5	1676	5	US-09-997-514-263			Sequence 263, App
c	23	66.4	17.5	1676	5	US-09-989-728-263			Sequence 263, App
c	24	66.4	17.5	1676	5	US-09-997-349-263			Sequence 263, App
c	25	66.4	17.5	1676	5	US-09-997-653-263			Sequence 263, App
c	26	66.4	17.5	1676	5	US-09-989-293A-263			Sequence 263, App
c	27	66.4	17.5	2412	3	US-10-104-047-824			Sequence 824, App
c	28	65	17.2	2073	3	US-09-023-655-1385			Sequence 1385, Ap
c	29	65	17.2	2073	4	US-09-880-107-1601			Sequence 1601, Ap
c	30	65	17.2	2369	4	US-09-880-107-3277			Sequence 3277, Ap
c	31	65	17.2	5050	3	US-09-949-016-132			Sequence 132, App
c	32	64.4	17.0	31208	3	US-09-852-067-3			Sequence 3, Appli
c	33	64.4	17.0	31208	3	US-10-338-691-3			Sequence 3, Appli
c	34	64.2	16.9	1185	3	US-09-023-655-1270			Sequence 1270, Ap
c	35	64.2	16.9	2367	3	US-09-949-016-4207			Sequence 4207, Ap
	36	55.2	14.6	285	3	US-09-020-956-153			Sequence 153, App
	37	55.2	14.6	285	3	US-09-030-607-153			Sequence 153, App
	38	55.2	14.6	285	3	US-09-439-313-153			Sequence 153, App
	39	55.2	14.6	285	3	US-09-352-616A-153			Sequence 153, App
	40	55.2	14.6	285	3	US-09-232-149A-153			Sequence 153, App
	41	55.2	14.6	285	3	US-09-159-812-153			Sequence 153, App
	42	55.2	14.6	285	3	US-09-636-215-153			Sequence 153, App
	43	55.2	14.6	285	3	US-09-685-166A-153			Sequence 153, App
	44	55.2	14.6	285	3	US-09-115-453-153			Sequence 153, App
	45	55.2	14.6	285	3	US-09-688-489-153			Sequence 153, App

## ALIGNMENTS

## RESULT 1

US-09-799-451-109/c

; Sequence 109, Application US/09799451

; Patent No. 6783969

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

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OM nucleic - nucleic search, using sw model

```
Run on:      October 3, 2006, 19:21:59 ; Search time 1456 Seconds
              (without alignments)
              3198.498 Million cell updates/sec
```

Title: US-10-714-389-52  
Perfect score: 379  
Sequence: 1 actttgccaaagcagtaaaag.....ttcaggtatgagtcacaggt 379

Scoring table: IDENTITY\_NUC .  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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```
Post-processing: Minimum Match 0% .
                  Maximum Match 100%
                  Listing first 45 summaries
```

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Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
```



Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	379	100.0	379	3	US-09-778-320-52	Sequence 52, Appl
2	379	100.0	379	3	US-09-910-689-52	Sequence 52, Appl
3	379	100.0	379	6	US-10-010-742-52	Sequence 52, Appl
4	379	100.0	379	8	US-10-714-389-52	Sequence 52, Appl
5	379	100.0	379	8	US-10-717-296-52	Sequence 52, Appl
c 6	379	100.0	598	9	US-10-357-930-24431	Sequence 24431, A
c 7	379	100.0	598	9	US-10-357-930-28061	Sequence 28061, A
c 8	379	100.0	870	6	US-10-198-846-4883	Sequence 4883, Ap
c 9	379	100.0	963	3	US-09-910-689-303	Sequence 303, App
c 10	379	100.0	963	6	US-10-010-742-303	Sequence 303, App
c 11	379	100.0	963	8	US-10-717-296-303	Sequence 303, App
c 12	379	100.0	1299	6	US-10-198-846-10784	Sequence 10784, A
c 13	379	100.0	1518	3	US-09-910-689-305	Sequence 305, App
c 14	379	100.0	1518	6	US-10-010-742-305	Sequence 305, App
c 15	379	100.0	1518	6	US-10-067-668-3	Sequence 3, Appli
c 16	379	100.0	1518	6	US-10-175-696-3	Sequence 3, Appli
c 17	379	100.0	1518	8	US-10-776-871-3	Sequence 3, Appli
c 18	379	100.0	1518	8	US-10-717-296-305	Sequence 305, App
c 19	379	100.0	1548	8	US-10-717-296-312	Sequence 312, App
c 20	379	100.0	1586	8	US-10-181-108-35	Sequence 35, Appl
c 21	379	100.0	1586	13	US-11-079-743-35	Sequence 35, Appl
c 22	379	100.0	1598	3	US-09-910-689-302	Sequence 302, App
c 23	379	100.0	1598	6	US-10-010-742-302	Sequence 302, App
c 24	379	100.0	1598	8	US-10-717-296-302	Sequence 302, App
c 25	379	100.0	1894	8	US-10-058-270A-1	Sequence 1, Appli
c 26	379	100.0	1975	6	US-10-067-668-1	Sequence 1, Appli
c 27	379	100.0	1975	6	US-10-175-696-1	Sequence 1, Appli
c 28	379	100.0	1975	8	US-10-776-871-1	Sequence 1, Appli
c 29	379	100.0	2015	3	US-09-910-689-304	Sequence 304, App
c 30	379	100.0	2015	6	US-10-010-742-304	Sequence 304, App
c 31	379	100.0	2015	8	US-10-296-606-23	Sequence 23, Appl
c 32	379	100.0	2015	8	US-10-717-296-304	Sequence 304, App
c 33	379	100.0	2020	6	US-10-227-884-29	Sequence 29, Appl
c 34	379	100.0	2020	6	US-10-230-163-29	Sequence 29, Appl
c 35	379	100.0	2020	6	US-10-230-338-29	Sequence 29, Appl
c 36	379	100.0	2020	6	US-10-218-631-29	Sequence 29, Appl
c 37	379	100.0	2020	6	US-10-230-414-29	Sequence 29, Appl
c 38	379	100.0	2020	6	US-10-232-224-29	Sequence 29, Appl
c 39	379	100.0	2020	6	US-10-216-159A-29	Sequence 29, Appl
c 40	379	100.0	2020	6	US-10-218-849-29	Sequence 29, Appl
c 41	379	100.0	2020	6	US-10-227-873-29	Sequence 29, Appl
c 42	379	100.0	2020	6	US-10-227-883-29	Sequence 29, Appl
c 43	379	100.0	2020	6	US-10-219-076-29	Sequence 29, Appl
c 44	379	100.0	2020	6	US-10-230-434-29	Sequence 29, Appl
c 45	379	100.0	2020	6	US-10-219-003-29	Sequence 29, Appl

## ALIGNMENTS

RESULT 1

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OM nucleic - nucleic search, using sw model

```
Run on:      October  3, 2006, 19:25:52 ; Search time 157 Seconds
              (without alignments)
              4454.578 Million cell updates/sec
```

Title: US-10-714-389-52  
Perfect score: 379  
Sequence: 1 actttgccaaagcagtaaaagq.....ttcaggtatgagtcacaggg 379

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2370645 seqs, 922650133 residues

Total number of hits satisfying chosen parameters: . 4741290

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Published_Applications_NA_New:*
1:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
9:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
10:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		%		Query							
No.	Score	Match	Length	DB	ID	Description					
c	1	379	100.0	1906	6	US-10-540-310-3	Sequence 3, Appli				
c	2	363	95.8	2608	8	US-11-293-697-1857	Sequence 1857, Ap				
c	3	154.6	40.8	1555	8	US-11-266-748A-367721	Sequence 367721,				
	4	154.6	40.8	1555	8	US-11-266-748A-451100	Sequence 451100,				
c	5	154.6	40.8	2349	8	US-11-293-697-2301	Sequence 2301, Ap				
c	6	154.6	40.8	2382	8	US-11-266-748A-56478	Sequence 56478, A				
	7	154	40.6	1000	8	US-11-266-748A-203310	Sequence 203310,				
	8	154	40.6	1000	8	US-11-266-748A-283212	Sequence 283212,				
c	9	154	40.6	1000	8	US-11-266-748A-309852	Sequence 309852,				
	10	154	40.6	1000	8	US-11-266-748A-392920	Sequence 392920,				
c	11	154	40.6	1000	8	US-11-266-748A-483638	Sequence 483638,				
	12	154	40.6	193471	8	US-11-266-748A-23901	Sequence 23901, A				
c	13	114.4	30.2	2376	8	US-11-293-697-2332	Sequence 2332, Ap				
c	14	111.4	29.4	1558	8	US-11-266-748A-78471	Sequence 78471, A				
	15	111.4	29.4	1558	8	US-11-266-748A-131282	Sequence 131282,				
	16	100.4	26.5	1754	8	US-11-266-748A-361338	Sequence 361338,				
c	17	100.4	26.5	1754	8	US-11-266-748A-444717	Sequence 444717,				
c	18	98.4	26.0	1000	8	US-11-266-748A-394439	Sequence 394439,				
	19	98.4	26.0	1000	8	US-11-266-748A-465485	Sequence 465485,				
c	20	95.2	25.1	779	8	US-11-266-748A-262386	Sequence 262386,				
	21	95.2	25.1	779	8	US-11-266-748A-322903	Sequence 322903,				
c	22	94	24.8	877	8	US-11-266-748A-214290	Sequence 214290,				
c	23	93	24.5	1000	8	US-11-266-748A-293498	Sequence 293498,				
	24	93	24.5	1000	8	US-11-266-748A-344927	Sequence 344927,				
	25	89	23.5	600	8	US-11-266-748A-102267	Sequence 102267,				
c	26	89	23.5	600	8	US-11-266-748A-155078	Sequence 155078,				
	27	79.8	21.1	947	8	US-11-266-748A-186910	Sequence 186910,				
c	28	79.8	21.1	947	8	US-11-266-748A-241605	Sequence 241605,				
c	29	75	19.8	2608	8	US-11-293-697-1514	Sequence 1514, Ap				
c	30	69.8	18.4	2950	8	US-11-266-748A-24706	Sequence 24706, A				
c	31	66.6	17.6	2360	8	US-11-266-748A-57526	Sequence 57526, A				
c	32	66.4	17.5	1000	8	US-11-266-748A-402012	Sequence 402012,				
	33	66.4	17.5	1000	8	US-11-266-748A-473058	Sequence 473058,				
c	34	66.4	17.5	1676	6	US-10-196-749-203	Sequence 203, App				
c	35	66.4	17.5	1676	8	US-11-101-316-53	Sequence 53, Appl				
c	36	66.4	17.5	1676	9	US-11-376-673-53	Sequence 53, Appl				
c	37	66.4	17.5	1694	8	US-11-266-748A-56537	Sequence 56537, A				
c	38	65	17.2	5050	8	US-11-266-748A-22281	Sequence 22281, A				
c	39	65	17.2	5050	8	US-11-266-748A-57232	Sequence 57232, A				
c	40	64.8	17.1	1212	8	US-11-266-748A-250041	Sequence 250041,				
c	41	64.8	17.1	1212	8	US-11-266-748A-274755	Sequence 274755,				
	42	64.8	17.1	1212	8	US-11-266-748A-310558	Sequence 310558,				
c	43	62	16.4	1000	8	US-11-266-748A-408223	Sequence 408223,				
	44	62	16.4	1000	8	US-11-266-748A-479269	Sequence 479269,				
c	45	55.2	14.6	876	8	US-11-266-748A-208902	Sequence 208902,				

## ALIGNMENTS

## RESULT 1

US-10-540-310-3/c

; Sequence 3, Application US/10540310

; Publication No. US20060166212A1

; GENERAL INFORMATION:

; APPLICANT: Avalon Pharmaceuticals, Inc.

; TITLE OF INVENTION: Breast Specific Protein Expressed in Cancer and Methods of

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OM nucleic - nucleic search, using sw model

```
Run on:      October 3, 2006, 18:54:43 ; Search time 4460 Seconds
              (without alignments)
              4751.889 Million cell updates/sec
```

Title: US-10-714-389-52  
Perfect score: 379  
Sequence: 1 acttttccaaagcagtaaagg.....ttcaggtatgagtcagggt 379

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries.
```

```
Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
c	1	154.6	40.8	770	2	BI913122	BI913122 603179852
c	2	154.6	40.8	1335	14	AY408468	AY408468 Homo sapi
c	3	149.2	39.4	559	9	DA362614	DA362614 DA362614
	4	141	37.2	623	1	AA193450	AA193450 zr40e07.r
c	5	140.4	37.0	1329	14	AY408470	AY408470 Mus muscu
c	6	140.4	37.0	3860	6	AK038526	AK038526 Mus muscu
c	7	128.6	33.9	628	4	BX272921	BX272921 BX272921
c	8	128.6	33.9	651	4	BX267843	BX267843 BX267843
c	9	128.6	33.9	676	5	CD216415	CD216415 pgp2n.pk0
c	10	125.6	33.1	786	5	CF547569	CF547569 AGENCOURT
c	11	124	32.7	869	10	DR860522	DR860522 JGI_CABG5
c	12	124	32.7	874	9	CX967511	CX967511 JGI_CAAP2
c	13	124	32.7	1642	6	BC054308	BC054308 Xenopus 1
	14	121	31.9	567	7	BF509149	BF509149 UI-H-BI4-
c	15	119.8	31.6	218	11	AY758967	AY758967 CH255-13m
c	16	119.8	31.6	556	5	CD734809	CD734809 4048891 1
c	17	119.2	31.5	735	3	BU243372	BU243372 603778833
c	18	118.2	31.2	839	3	BU227845	BU227845 603947881
c	19	116.6	30.8	824	9	CX966129	CX966129 JGI_CAAP1
c	20	116	30.6	792	2	BG193485	BG193485 RST12619
c	21	115.2	30.4	767	5	CJ023895	CJ023895 CJ023895
c	22	115	30.3	655	2	BJ909012	BJ909012 BJ909012
	23	114.4	30.2	817	10	DR860523	DR860523 JGI_CABG5
c	24	114	30.1	773	2	BG461834	BG461834 RST44771
c	25	112	29.6	740	3	BP435575	BP435575 BP435575
c	26	112	29.6	813	3	BP435822	BP435822 BP435822
c	27	112	29.6	841	5	CJ025855	CJ025855 CJ025855
c	28	112	29.6	870	5	CJ022965	CJ022965 CJ022965
c	29	112	29.6	932	3	BQ881161	BQ881161 AGENCOURT
c	30	111.4	29.4	769	4	CA487879	CA487879 AGENCOURT
c	31	111.4	29.4	1038	2	BG291597	BG291597 602388704
c	32	111.2	29.3	252	2	BG204180	BG204180 RST23576
c	33	110.4	29.1	808	5	CJ022616	CJ022616 CJ022616
c	34	109.6	28.9	741	4	CB599980	CB599980 AGENCOURT
c	35	109.6	28.9	759	4	CB950823	CB950823 AGENCOURT
c	36	109.6	28.9	779	4	CB600740	CB600740 AGENCOURT
c	37	108.8	28.7	735	5	CK471537	CK471537 AGENCOURT
c	38	108.8	28.7	746	5	CK364271	CK364271 AGENCOURT
c	39	108.8	28.7	805	10	DR428109	DR428109 naw50f07.
c	40	108.8	28.7	864	8	CO554538	CO554538 AGENCOURT
c	41	108	28.5	570	4	CB601086	CB601086 AGENCOURT
c	42	108	28.5	622	2	BG971712	BG971712 602838239
c	43	108	28.5	640	2	BG971106	BG971106 602837813
c	44	108	28.5	651	7	BE851329	BE851329 uw94g07.y
c	45	108	28.5	747	4	CB953130	CB953130 AGENCOURT

## ALIGNMENTS

## RESULT 1

BI913122/c

LOCUS

BI913122

770 bp

mRNA

linear

EST 16-OCT-2001